● PRINTER RUSH ●
(PTO ASSISTANCE)

Application :	09/755320	Examiner :	Saoud	GAU :	1647
From:	thc	Location: (IDC) FMF FDC		Date:	1/6/06

Tracking #: 0100 3167   Week Date: 8/15/05

DOC CODE	DOC DATE	MISCELLANEOUS
☐ 1449	_____	☐ Continuing Data
☐ IDS	_____	☐ Foreign Priority
☐ CLM	_____	☐ Document Legibility
☐ IIFW	_____	☐ Fees
☐ SRFW	_____	☐ Other
☐ DRW	_____	
☐ OATH	_____	
☐ 312	_____	
☒ SPEC	_____	

[RUSH] MESSAGE: Sequence listing has never been received electronically. Please take disk containing computer readable form or letter requesting transfer from parent to Mark Spencer in STIC.

Thank you.

[XRUSH] RESPONSE: CRF transferred from Parent.

INITIALS: CW

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.

REV 10/04

RAW SEQUENCE LISTING   DATE: 01/26/2006
PATENT APPLICATION: US/09/755,320   TIME: 10:10:26

Input Set : N:\Crf3\RULE60\09755320.raw.txt
Output Set: N:\CRF4\01262006\I755320.raw

SEQUENCE LISTING

```
   3 (1) GENERAL INFORMATION:
   5     (i) APPLICANT: Gorski, David H.
   6                    Walsh, Kenneth
   8    (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
  10   (iii) NUMBER OF SEQUENCES: 19
  12    (iv) CORRESPONDENCE ADDRESS:
  13         (A) ADDRESSEE: Calfee, Halter, and Griswold
  14         (B) STREET: 800 Superior Avenue
  15         (C) CITY: Cleveland
  16         (D) STATE: Ohio
  17         (E) COUNTRY: U.S.A.
  18         (F) ZIP: 44114-2688
  20     (v) COMPUTER READABLE FORM:
  21         (A) MEDIUM TYPE: Floppy disk
  22         (B) COMPUTER: IBM PC compatible
  23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  24         (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
  26    (vi) CURRENT APPLICATION DATA:
C--> 27     (A) APPLICATION NUMBER: US/09/755,320
C--> 28     (B) FILING DATE: 05-Jan-2001
W--> 34     (C) CLASSIFICATION: 435
  31   (vii) PRIOR APPLICATION DATA:
  32         (A) APPLICATION NUMBER: US/08/203,532
  33         (B) FILING DATE: 24-Feb-1994
  36  (viii) ATTORNEY/AGENT INFORMATION:
  37         (A) NAME: Golrick, Mary E.
  38         (B) REGISTRATION NUMBER: 34829
  39         (C) REFERENCE/DOCKET NUMBER: 22311/00114
  41    (ix) TELECOMMUNICATION INFORMATION:
  42         (A) TELEPHONE: (216) 622-8200
  43         (B) TELEFAX: (216) 241-0816
  44         (C) TELEX: 980499
  47 (2) INFORMATION FOR SEQ ID NO: 1:
  49     (i) SEQUENCE CHARACTERISTICS:
  50         (A) LENGTH: 2244 base pairs
  51         (B) TYPE: nucleic acid
  52         (C) STRANDEDNESS: both
  53         (D) TOPOLOGY: linear
  55    (ii) MOLECULE TYPE: cDNA
  57   (iii) HYPOTHETICAL: NO
  59    (iv) ANTI-SENSE: NO
  62    (ix) FEATURE:
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63          (A) NAME/KEY: CDS
64          (B) LOCATION: 197..1108
67    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 GTCAAGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT      60
71 CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT     120
73 AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGGAAG     180
75 CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC         229
76                Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
77                 1                 5                   10
79 CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG       277
80 Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
81          15              20                  25
83 GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA       325
84 Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
85          30              35                  40
87 TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG       373
88 Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
89       45              50                  55
91 TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC       421
92 Phe Ala Ser Gln His His Arg Gly His His His His His His His His
93  60              65                  70                  75
95 CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG       469
96 His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
97              80                  85                  90
99 CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT       517
100 His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
101             95                  100                 105
103 TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT      565
104 Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro
105             110                 115                 120
107 CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC      613
108 Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr
109     125                 130                 135
111 GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC      661
112 Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro
113 140             145                 150                 155
115 GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA      709
116 Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser
117             160                 165                 170
119 GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG      757
120 Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg
121             175                 180                 185
123 AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA      805
124 Arg Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala
125         190                 195                 200
127 GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA      853
128 Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile
129 205                 210                 215
131 GCG GTG AAC CTA GAC CTC ACT GAA AGA CAG GTG AAA GTG TGG TTC CAG      901
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132 Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln
133 220               225               230               235
135 AAC AGG AGA ATG AAG TGG AAG CGG GTC AAG GGG GGA CAA CAA GGA GCT      949
136 Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala
137                   240               245               250
139 GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT      997
140 Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu
141               255               260               265
143 CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG     1045
144 Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly
145           270               275               280
147 GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG     1093
148 Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu
149       285               290               295
151 CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC        1145
152 His Ala His Leu
153 300
155 ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTTG   1205
157 CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC   1265
159 ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA   1325
161 AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA   1385
163 AAATTAAATT GCTACCAAGA GCAAACTCGG TAAGACATTT TGACTCAAGT TGTCTCCAGA   1445
165 GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC   1505
167 TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA   1565
169 AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG   1625
171 AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA   1685
173 TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT   1745
175 TTTATACATT TTTTTGTCAG TCAGAGACAT CAGTATGTGC TTACTTGTGT TCAAGTAGAG   1805
177 GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG   1865
179 TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC   1925
181 TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA   1985
183 GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT   2045
185 CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA   2105
187 CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA   2165
189 AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA   2225
191 AAAAAAAGTT AAATAAATG                                               2244
194 (2) INFORMATION FOR SEQ ID NO: 2:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 303 amino acids
198          (B) TYPE: amino acid
199          (D) TOPOLOGY: linear
201      (ii) MOLECULE TYPE: protein
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
205 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
206   1               5               10              15
208 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
209             20              25              30
211 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
212         35              40              45
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214 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
215      50              55                  60
217 His Arg Gly His His His His His His His His His His His His Gln
218 65               70               75               80
220 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
221              85              90                  95
223 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
224             100             105             110
226 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
227         115             120             125
229 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
230     130             135             140
232 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
233 145             150             155             160
235 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
236             165             170             175
238 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
239         180             185             190
241 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
242     195             200             205
244 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
245     210             215             220
247 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
248 225             230             235             240
250 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
251             245             250             255
253 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
254             260             265             270
256 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
257         275             280             285
259 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
260     290             295             300
263 (2) INFORMATION FOR SEQ ID NO: 3:
265      (i) SEQUENCE CHARACTERISTICS:
266          (A) LENGTH: 941 base pairs
267          (B) TYPE: nucleic acid
268          (C) STRANDEDNESS: both
269          (D) TOPOLOGY: linear
271     (ii) MOLECULE TYPE: cDNA
273    (iii) HYPOTHETICAL: NO
275     (iv) ANTI-SENSE: NO
278     (ix) FEATURE:
279          (A) NAME/KEY: CDS
280          (B) LOCATION: 33..941
283     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
285 GTCTTCTACC TGGAACCCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC        53
286                                    Met Glu His Pro Leu Phe Gly
287                                     1               5
289 TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC      101
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290 Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser
291          10              15                  20
293 CAA TCC TCT CTC GCC CTC CAT GGA AGA TCT GAC CAT ATG TCT TAC CCC        149
294 Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro
295     25              30                  35
297 GAG CTC TCT ACT TCT TCC TCA TCT TGC ATA ATC GCG GGA TAC CCC AAC        197
298 Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn
299 40                  45              50                  55
301 GAA GAG GAC ATG TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC        245
302 Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His
303              60              65                  70
305 CAC CAC CAC CAT CAC CAC CAT CAG CAG CAG CAG CAC CAG GCT CTG CAA        293
306 His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln
307              75              80                  85
309 ACC AAC TGG CAC CTC CCG CAG ATG TCT TCC CCA CCG AGT GCG GCT CGG        341
310 Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg
311          90              95                  100
313 CAT AGC CTC TGC CTC CAG CCC GAC TCT GGA GGG CCC CCA GAG TTG GGG        389
314 His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly
315     105             110                 115
317 AGC AGC CCG CCC GTC CTG TGC TCC AAC TCT TCC AGC TTG GGC TCC AGC        437
318 Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser
319 120             125                 130                 135
321 ACC CCG ACT GGG GCC GCG TGC GCG CCG GGG GAC TAC GGC CGC CAG GCA        485
322 Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala
323             140                 145                 150
325 CTG TCA CCT GCG GAG GCG GAG AAG CGA AGC GGC GGC AAG AGG AAA AGC        533
326 Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser
327             155                 160                 165
329 GAC AGC TCA GAC TCC CAG GAA GGA AAT TAC AAG TCA GAA GTC AAC AGC        581
330 Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser
331         170                 175                 180
333 AAA CCC AGG AAA GAA AGG ACA GCA TTT ACC AAA GAG CAA ATC AGA GAA        629
334 Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu
335     185                 190                 195
337 CTT GAA GCA GAA TTT GCC CAT CAT AAT TAT CTC ACC AGA CTG AGG CGA        677
338 Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg
339 200                 205                 210                 215
341 TAC GAG ATA GCA GTG AAT CTG GAT CTC ACT GAA AGA CAG GTA AAA GTC        725
342 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
343             220                 225                 230
345 TGG TTC CAA AAC AGG CGG ATG AAG TGG AAG AGG GTA AAG GGT GGA CAG        773
346 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
347             235                 240                 245
349 CAA GGA GCT GCG GCT CGG GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA        821
350 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
351             250                 255                 260
353 ACA CTT CTC CCA TCA GAG CTG TCG GGA ATT GGT GCA GCC ACC CTC CAG        869
354 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
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VERIFICATION SUMMARY   DATE: 01/26/2006
PATENT APPLICATION: US/09/755,320 TIME: 10:10:27

Input Set : N:\Crf3\RULE60\09755320.raw.txt
Output Set: N:\CRF4\01262006\I755320.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)